



IFWO

RAW SEQUENCE LISTING

DATE: 09/01/2004

PATENT APPLICATION: US/10/825,568

TIME: 13:06:01

Input Set : N:\Crf3\RULE60\10825568.raw

Output Set: N:\CRF4\09012004\J825568.raw

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1.<110> APPLICANT: Brian T. Chait
2      Darin R. Latimer
3      Paul M. Lizardi
4      Eric R. Kershner
5      Jon S. Morrow
6      Matthew E. Roth
7      Martin J. Mattessich
8      Kevin J. McConnell
9 <120> TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
10 <130> FILE REFERENCE: 01173.0003U2
11 <140> CURRENT APPLICATION NUMBER: US/10/825,568
12 <141> CURRENT FILING DATE: 2004-04-14
13 <150> PRIOR APPLICATION NUMBER: US/09/929,266
14 <151> PRIOR FILING DATE: 2001-08-13
15 <150> PRIOR APPLICATION NUMBER: 60/224,939
16 <151> PRIOR FILING DATE: 2000-08-11
17 <150> PRIOR APPLICATION NUMBER: 60/283,498
18 <151> PRIOR FILING DATE: 2000-04-12
19 <160> NUMBER OF SEQ ID NOS: 33
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 12
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Artificial Sequence; Note=synthetic
28      construct
29 <400> SEQUENCE: 1
30      Cys Gly Gly Gly Gly Asp Pro Gly Gly Gly Gly Arg
31      1             5             10
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 11
35 <212> TYPE: PRT
36 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Description of Artificial Sequence; Note=synthetic
39      construct
40 <400> SEQUENCE: 2
41      Ala Gly Ser Leu Asp Pro Ala Gly Ser Leu Arg
42      1             5             10
44 <210> SEQ ID NO: 3
45 <211> LENGTH: 13
46 <212> TYPE: PRT

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47 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Description of Artificial Sequence; Note=synthetic
50     construct
51 <400> SEQUENCE: 3
52     Ala Gly Ser Met Leu Asp Pro Ala Gly Ser Met Leu Arg
53         1             5             10
55 <210> SEQ ID NO: 4
56 <211> LENGTH: 11
57 <212> TYPE: PRT
58 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Description of Artificial Sequence; Note=synthetic
61     construct
62 <400> SEQUENCE: 4
63     Ala Gly Ser Leu Ala Asp Pro Gly Ser Leu Arg
64         1             5             10
66 <210> SEQ ID NO: 5
67 <211> LENGTH: 11
68 <212> TYPE: PRT
69 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: Description of Artificial Sequence; Note=synthetic
72     construct
73 <400> SEQUENCE: 5
74     Ala Leu Ser Leu Ala Asp Pro Gly Ser Gly Arg
75         1             5             10
77 <210> SEQ ID NO: 6
78 <211> LENGTH: 11
79 <212> TYPE: PRT
80 <213> ORGANISM: Artificial Sequence
81 <220> FEATURE:
82 <223> OTHER INFORMATION: Description of Artificial Sequence; Note=synthetic
83     construct
84 <400> SEQUENCE: 6
85     Ala Leu Ser Leu Gly Asp Pro Ala Ser Gly Arg
86         1             5             10
88 <210> SEQ ID NO: 7
89 <211> LENGTH: 11
90 <212> TYPE: PRT
91 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Description of Artificial Sequence; Note=synthetic
94     construct
95 <400> SEQUENCE: 7
96     Ala Gly Ser Asp Pro Leu Ala Gly Ser Leu Arg
97         1             5             10
99 <210> SEQ ID NO: 8
100 <211> LENGTH: 11

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101 <212> TYPE: PRT
102 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Description of Artificial Sequence; Note=synthetic
105 construct
106 <400> SEQUENCE: 8
107 Ala Asp Pro Gly Ser Leu Ala Gly Ser Leu Arg
108 1 5 10
110 <210> SEQ ID NO: 9
111 <211> LENGTH: 357
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
114 <400> SEQUENCE: 9
115 Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr Glu Cys Ile Ala
116 1 5 10 15
117 Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
118 20 25 30
119 Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
120 35 40 45
121 Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
122 50 55 60
123 Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
124 65 70 75 80
125 Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
126 85 90 95
127 Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
128 100 105 110
129 Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
130 115 120 125
131 Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
132 130 135 140
133 Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
134 145 150 155 160
135 Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
136 165 170 175
137 Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
138 180 185 190
139 Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
140 195 200 205
141 Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
142 210 215 220
143 Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
144 225 230 235 240
145 Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
146 245 250 255
147 Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
148 260 265 270
149 Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
150 275 280 285

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151    Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
152          290                      295                      300
153    Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
154    305                      310                      315                      320
155    Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
156          325                      330                      335
157    Lys Glu Ala Ser Thr Pro Arg Thr Arg Ala Ser Cys Gln Ser Ser Gly
158          340                      345                      350
159    Gln Pro Leu Arg Pro
160          355
162 <210> SEQ ID NO: 10
163 <211> LENGTH: 536
164 <212> TYPE: PRT
165 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 10
167    Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
168    1                      5                      10                      15
169    Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
170          20                      25                      30
171    Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
172          35                      40                      45
173    Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
174          50                      55                      60
175    Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
176    65                      70                      75                      80
177    Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
178          85                      90                      95
179    Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
180          100                     105                     110
181    Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
182          115                     120                     125
183    Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
184          130                     135                     140
185    Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
186    145                     150                     155                     160
187    Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
188          165                     170                     175
189    Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
190          180                     185                     190
191    Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
192          195                     200                     205
193    Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
194          210                     215                     220
195    Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
196    225                     230                     235                     240
197    Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
198          245                     250                     255
199    Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
200          260                     265                     270

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201   Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
202           275                      280                      285
203   Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
204           290                      295                      300
205   Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
206           305                      310                      315                      320
207   Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
208           325                      330                      335
209   Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
210           340                      345                      350
211   Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
212           355                      360                      365
213   Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
214           370                      375                      380
215   Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
216           385                      390                      395                      400
217   Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
218           405                      410                      415
219   Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
220           420                      425                      430
221   Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
222           435                      440                      445
223   Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
224           450                      455                      460
225   Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
226           465                      470                      475                      480
227   Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
228           485                      490                      495
229   Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
230           500                      505                      510
231   Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
232           515                      520                      525
233   Gln Tyr Gln Pro Gly Glu Asn Leu
234           530                      535
236 <210> SEQ ID NO: 11
237 <211> LENGTH: 13
238 <212> TYPE: PRT
239 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence; Note=synthetic
242   construct
243 <400> SEQUENCE: 11
244   Cys Gly Ala Gly Ser Asp Pro Leu Ala Gly Ser Leu Arg
245       1             5             10
247 <210> SEQ ID NO: 12
248 <211> LENGTH: 10
249 <212> TYPE: PRT
250 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/01/2004
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Input Set : N:\Crf3\RULE60\10825568.raw
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:24; Xaa Pos. 3,4,5,6,7,10,11,12,13,14

Seq#:25; Xaa Pos. 1,2,3,4,5,6,7,8,9,12,13,14,15,16,17,18,19,20,21,24,25,26

Seq#:25; Xaa Pos. 27,28,29,30,32,33,34,35

Seq#:26; Xaa Pos. 1,2,3,4,5,6,7,8,9,12,13,14,15,16,17,18,19,20,21,23,24,25

Seq#:26; Xaa Pos. 26,27,28,29,31,32,33,34

VERIFICATION SUMMARY

DATE: 09/01/2004

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Input Set : N:\Crf3\RULE60\10825568.raw

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L:382 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:385 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:396 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:399 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25
L:400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
M:341 Repeated in SeqNo=25
L:414 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:417 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
M:341 Repeated in SeqNo=26